

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: RBS
(B) LOCATION: 24..28

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 38..184

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 38..125

(ix) FEATURE:

(A) NAME/KEY: primer_bind
(B) LOCATION: 114..144

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION: 114..119
(D) OTHER INFORMATION: /label= Restrict_site

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATCTTGGTAT CACAACTAA TTTGGAGGTT GGTATAT ATG AAA AAA CAA ATT TTA 55
Met Lys Lys Gln Ile Leu
1 5

AAA GGG TTG GTT ATA GTT GTT TGT TTA TCT GGG GCA ACA TTT TTC TCA 103
Lys Gly Leu Val Ile Val Val Cys Leu Ser Gly Ala Thr Phe Phe Ser
10 15 20

ACA CCA CAA CAA GCT TCT GCT GTA AAT TAT GGT AAT GGT GTT TCT TGC 151
Thr Pro Gln Gln Ala Ser Ala Val Asn Tyr Gly Asn Gly Val Ser Cys
25 30 35

AGT AAA ACA AAA TGT TCA GTT AAC TGG GGA CAA 184
Ser Lys Thr Lys Cys Ser Val Asn Trp Gly Gln
40 45

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 49 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

10 Met Lys Lys Gln Ile Leu Lys Gly Leu Val Ile Val Val Cys Leu Ser
 1 5 10 15
Gly Ala Thr Phe Phe Ser Thr Pro Gln Gln Ala Ser Ala Val Asn Tyr
 20 25 30
15 Gly Asn Gly Val Ser Cys Ser Lys Thr Lys Cys Ser Val Asn Trp Gly
 35 40 45
Gln

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 4290 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vii) IMMEDIATE SOURCE:
 (B) CLONE: Leucocin A genes

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

40 AATTTTGGCC CATGCTGCAT GATATTTTGA CTACCAAAAA ATATGCCGTGT TCGTACTTTC 60
AATGTTGATA ATTTTTTTTAA AGATAATTCC TCTGACAAAG CTAGTTATAT TAATTTCTTT 120
CAAGAGTTAA ATATTTCTCA ACTGCCTTCT TTAATTTTTA CTAATGGAAA CATGGACTAT 180
45 AAACGATTAT CAATTTATAC AATTAAAACA CCAATAAATG CATGGATTAC TGCTATTAAT 240
GACGAATTAA TTTCAAACA TTCCAAGCAA TCATCAACAA ATTAAAAATG GTTAAGGTCA 300
50 AAATGTTTCA AAAAAGAATA AATTATATCG CACAAGTAGA TGAACGTGAT TGTGGTGTG 360
CTGCACTCGC TATGGTTTTA ACTCATTACA AAACACGCCT GTCCTTAGCC AACTACGGG 420
ACCTGGCCAA AACTGACATG GAAGGAACGA CTGCTTTAGG CATTGTTAAA GCTGCGAATG 480

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	CGCTAGACTT	TGAAACCATG	CCGATCCAGG	CTGATTTGAG	TTTATTCGAT	AAAAAGGATT	540
	TACCOCTATCC	TTTTATCGCC	CATGTCATTA	AAGACGGTAA	ATACCCGCAT	TATTATGTAG	600
5	TTTATGGGAT	CAAAGGTGAT	CAGCTATTAA	TCGCTGATCC	AGATAATACC	GTTGGTAAAA	660
	ATAAAATGAC	AAAAGCGCAT	TTTAATGAGG	AGTGGACCGG	TGTGTCCATT	TTTATTGCGC	720
10	CCAATCCAAC	CTACAAGCCA	ACAAAGGATA	AAAAGCGTTC	CTTGACTTCT	TTTATTCCAG	780
	TGATTACGCG	TCAAAAATTA	TTAGTTATCA	ATATTGTCAT	TGCTGCCTTG	TTGGTTACCC	840
	TAGTGAGTAT	TTTAGGATCA	TATTATTTGC	AAGGTATCAT	TGATACCTAT	ATCCCCGATA	900
15	ACATGAAAAA	CACCCTAGGG	ATTGTGTCAC	TAGGGCTTAT	TTTTGCGTAT	GTTATCCAAC	960
	AACTGCTCTC	TTATGCCAGA	GATTATTTAT	TAATTGTCAT	GGGGCAACGC	CTCTCAATTG	1020
20	ATATTATTTT	GTCTTATATC	AAACACATTT	TTGAACTGCC	AATGTCTTTT	TTCGCGACGC	1080
	GTCGTACCGG	TGAAATTGTG	AGCCGTTTTA	CGGACGCTAA	TGCCATTATT	GAAGCCCTGG	1140
	CAAGCACGAT	GTTATCTGTA	TTTTTAGACT	TAGGAATTTT	GGTCATTGTT	GGCACAGTGC	1200
25	TAGTGGTTCA	AAATTCAACC	TTGTTTCTGA	TTTCTCTGAT	TGCCATTCCG	GCTTATGCCC	1260
	TAGTGGTCTG	GCTCTTTATG	CGTCCTTTTT	CAAAGATGAA	TAATGACCAA	ATGCAAGCAG	1320
30	GTTCGATGTT	AAGTTCTTCC	ATTATTGAAG	ATATTAATGG	CGTTGAGACG	ATTAAAGCGC	1380
	TGAATAGTGA	AGAAACCGCC	TATCATAAAA	TTGATCATGA	ATTTGTCACT	TATTTAGAAA	1440
	AATCATTTGT	TTACGCTAAA	ACAGAAGCCA	CTCAAAATGC	GATTAAAAGC	CTCTTACAGC	1500
35	TCTCTTTAAA	TGTCGTGATC	TTATGGGTTG	GCGCACAACT	GGTCATGACC	AATAAAATTA	1560
	GTGTTGGTCA	ACTGATCACT	TACAATGCTT	TATTAGGATT	TTTTACAGAT	CCCTTGCAAA	1620
40	ATATTATTAA	TTTACAAACT	AAGCTCCAAC	AGGCCTCAGT	CGCTAATAAT	CGTTTGAACG	1680
	AAGTTTATTT	GGTTGATTCA	GAATTTAAAG	CTAGTCATCA	AATGACAGAA	AGCATTATGC	1740
	CCAATAGCTC	ATTAGTAGCC	GATCATATCA	CCTATAAATA	CGGTTTGGT	GCGCCAGCAA	1800
45	TTGATGATGT	TTCACTAACG	ATTACAGCCG	GTGAAAAAAT	CGCTTTGGTT	GGGATTAGTG	1860
	GATCAGGTAA	ATCAACTTTA	GTTAAATTGC	TGGTTAATTT	CTTTCAACCA	GAGTCAGGGA	1920
50	CAATTTCACT	AGGACAAACA	CCACTCGCCA	ATCTTGATAA	ACATGAGCTA	AGAGCACACA	1980
	TTAATTATTT	ACCACAAGAA	CCCTTTATAT	TTTCCGGTTC	AATTATGGAC	AACCTGTTAT	2040
	TGGGGGCTAA	GCCAGGGACA	ACCCAAGAAG	ATATTATCAG	GGCGGTAGAA	ATTGCTGAAA	2100

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	TTAAAGATGA TATTGAAAAA ATGTCGCAAG GATTTGGCAC TGAAC TCGCA GAAAGTGGCA	2160
	ATATTTTCGGG TGGTCAAAAA CAACGCATTG CTTTAGCTAG AGCCATTTTA GTCGATTCTC	2220
5	CGGTGCTGAT TTTAGATGAG TCAACCAGTA ATCTTGATGT TTTAACAGAA AAAAAGATTA	2280
	TTGATAATCT CATGCAGTTA ACCGAAAAAA CCATTATCTT TGTAGCGCAC CGCTTAACCA	2340
10	TTTCACAGCG AGTAGATCGT ATTCTAACCA TGCAAAACGG CAAAATTATC GAAGATGGCA	2400
	CGCATAATAC TCTGCTTAAT GCCGGTGGTT TCTACGCGTC ATTGTTTAAT CATTAGGAG	2460
	ACCTGATGTT TGATCCAAAA TACTTAGAAA GTGGCGAATT TTATCAACGT CGTTACCGCA	2520
15	ATTTTCCAAC TCTGATTATT GTGCCTATTT TTTTGTAGT CGTGT TATC ATTCTATTTA	2580
	GCCTATTTGC TAAGCGTGAA ATTGTTGTCA AAGCAAGTGG CGAAATTATT CCAGCCAAAG	2640
20	TGCTATCAGA TATCCAATCA ACCAGTAACA ATGCCATCGA TAGTAACCAA TTAAGTAAA	2700
	ATAAAGTGGT TAAAAAGGC GATACCTTAG TGACCTTTAC CAGTGGTAAT GAAAAATAT	2760
	CGTCTCAATT ACTGACGCAA CAACTTAATA ATCTTAACGA CCGTCTAAAA AGTCTTGATA	2820
25	CCTATAAGCA GAGTATTGTT AACGGACGTA GCGAATTTGG TGGCACAGAT CAATTTGGTT	2880
	ATGATAGTCT ATTCAACGGC TATATGGCGC AAGTTGATAC GTTGACGAGT GAATTTAATC	2940
30	AACAAAGTAG TGATAAACAA ACAGCTGATC AACAAAGCTAA TCATCAAATT GACGTTTTAA	3000
	AACAAGGTCA ATCTAAAAAC AATCAACAAT TAGCTAATTA TCAAGCTATT CTAACCAGTA	3060
	TTAATAGCAA CACTAAACCG ACTAATAATC CCTATCAAGC CATTTATGAT AATTATTCAG	3120
35	CCCAGTTAAA ATCAGCACAA ACAACTGATG ATAAAGATCA AGTCAAGCAA ACTGCCTTAA	3180
	GTAATGTACA ACAACAAATT GATCAATTAC AAACAACGAG TAGTTCGTAT GATAGTCAA	3240
40	TTGCTGGTAT TACAAAGAGT GGTCTTTTAT CTCAAAGCAG TACCTTAGAT AAAATCGCTG	3300
	ACTTGAAGCA ACAACAATA GCGAGTGCTC AAAAAGAAAT CAATGATCAG CAACAATCCT	3360
	TAGATGAGTT AAAAGCCAAG CAATCCTCTG CTAATGAGGA TTATCAAGAT ACGGTTATTA	3420
45	AAGCACCAGA AGATGGCATT TTACATTTAG CCACTGACAA AACTAAAATC AAGTATTTCC	3480
	CTAAAGGCAC AACCATTGCG CAAATTTATC CTAAACTGAC GCAAAAAACA GCTTTGAATG	3540
50	TTGAGTACTA TGTGCCTGCC AGTAATATTA TCGGCTTAAA GCAAAGACAA GCCATCCGTT	3600
	TTGTAGCAAA TCAAAATGTC ACGAAACCGC TCACCTTAAA CGGAACAATC AAAAGCATT	3660
	GTTCTGCACC AATAGCCAGT AAAGAGGGAT CCTTTTATAA ATTAGTCGCG ACGATTCAGG	3720

CTAGCAAAAT AGACCGTGAA CAGATTAAAT ATGGTCTTAA TGGTCGAATC ACAACCATAA 3780
AAGGGACTAA AACATGGTTT AATTATTATA AAGACATTGT TTTAGGTGAG AATAATTAGC 3840
5 TAGGAAGATA AACACAATTT TTAAACGTGT TTATCTTTTT TAGTCTCAAT GAAATTGTCG 3900
CCGAAGGTTT TTCTAGCCAA GTGGCAGGAC ACAGAAAAAT GATAGTTGCT ACTGAAGGGA 3960
10 AGTTCAACTG CCACCAAAAA TAGTAACCGC GCGACAGCCA ACCGCCACCA CAACAGTTAT 4020
GCTCGCCCGT GGTTATTATT ATCATTAACA CTCTTACGTC TTTCTATGAT ACTTTTGAGC 4080
CACATTCTTA TAATGCTGCA ATCGACCTTT TAGAAAATTG ATCTCATCAG AAATTTCTTT 4140
15 TAAGTGGTTA TCATCAGCAT GTTTACTAGC AATATTTAAT TCTTTAATCC TACGTTTAAT 4200
CAACTTAGTA GTTTTAGTAT CTTTCATGTA TTGATTATCT CAAAAAACA CCCAACAAGG 4260
GCAATCAGTT TGATTTGAGC AGAGGAAGCC 4290

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 717 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:
(B) CLONE: lcaC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Phe	Gln	Lys	Arg	Ile	Asn	Tyr	Ile	Ala	Gln	Val	Asp	Glu	Arg	Asp
1			5					10						15	
Cys	Gly	Val	Ala	Ala	Leu	Ala	Met	Val	Leu	Thr	His	Tyr	Lys	Thr	Arg
		20					25						30		
Leu	Ser	Leu	Ala	Lys	Leu	Arg	Asp	Leu	Ala	Lys	Thr	Asp	Met	Glu	Gly
		35				40					45				
Thr	Thr	Ala	Leu	Gly	Ile	Val	Lys	Ala	Ala	Asn	Ala	Leu	Asp	Phe	Glu
	50				55				60						
Thr	Met	Pro	Ile	Gln	Ala	Asp	Leu	Ser	Leu	Phe	Asp	Lys	Lys	Asp	Leu

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65	70	75	80
Pro Tyr Pro Phe Ile Ala His Val Ile Lys Asp Gly Lys Tyr Pro His	85	90	95
Tyr Tyr Val Val Tyr Gly Ile Lys Gly Asp Gln Leu Leu Ile Ala Asp	100	105	110
Pro Asp Asn Thr Val Gly Lys Asn Lys Met Thr Lys Ala His Phe Asn	115	120	125
Glu Glu Trp Thr Gly Val Ser Ile Phe Ile Ala Pro Asn Pro Thr Tyr	130	135	140
Lys Pro Thr Lys Asp Lys Lys Arg Ser Leu Thr Ser Phe Ile Pro Val	145	150	155
Ile Thr Arg Gln Lys Leu Leu Val Ile Asn Ile Val Ile Ala Ala Leu	165	170	175
Leu Val Thr Leu Val Ser Ile Leu Gly Ser Tyr Tyr Leu Gln Gly Ile	180	185	190
Ile Asp Thr Tyr Ile Pro Asp Asn Met Lys Asn Thr Leu Gly Ile Val	195	200	205
Ser Leu Gly Leu Ile Phe Ala Tyr Val Ile Gln Gln Leu Leu Ser Tyr	210	215	220
Ala Arg Asp Tyr Leu Leu Ile Val Met Gly Gln Arg Leu Ser Ile Asp	225	230	235
Ile Ile Leu Ser Tyr Ile Lys His Ile Phe Glu Leu Pro Met Ser Phe	245	250	255
Phe Ala Thr Arg Arg Thr Gly Glu Ile Val Ser Arg Phe Thr Asp Ala	260	265	270
Asn Ala Ile Ile Glu Ala Leu Ala Ser Thr Met Leu Ser Val Phe Leu	275	280	285
Asp Leu Gly Ile Leu Val Ile Val Gly Thr Val Leu Val Val Gln Asn	290	295	300
Ser Thr Leu Phe Leu Ile Ser Leu Ile Ala Ile Pro Ala Tyr Ala Leu	305	310	315
Val Val Trp Leu Phe Met Arg Pro Phe Ser Lys Met Asn Asn Asp Gln	325	330	335
Met Gln Ala Gly Ser Met Leu Ser Ser Ser Ile Ile Glu Asp Ile Asn	340	345	350
Gly Val Glu Thr Ile Lys Ala Leu Asn Ser Glu Glu Thr Ala Tyr His			

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	355		360		365	
	Lys Ile Asp His Glu Phe Val Thr Tyr Leu Glu Lys Ser Phe Val Tyr					
	370		375		380	
5	Ala Lys Thr Glu Ala Thr Gln Asn Ala Ile Lys Ser Leu Leu Gln Leu					
	385		390		395	400
10	Ser Leu Asn Val Val Ile Leu Trp Val Gly Ala Gln Leu Val Met Thr					
		405		410		415
	Asn Lys Ile Ser Val Gly Gln Leu Ile Thr Tyr Asn Ala Leu Leu Gly					
		420		425		430
15	Phe Phe Thr Asp Pro Leu Gln Asn Ile Ile Asn Leu Gln Thr Lys Leu					
		435		440		445
	Gln Gln Ala Ser Val Ala Asn Asn Arg Leu Asn Glu Val Tyr Leu Val					
		450		455		460
20	Asp Ser Glu Phe Lys Ala Ser His Gln Met Thr Glu Ser Ile Met Pro					
		465		470		475
	Asn Ser Ser Leu Val Ala Asp His Ile Thr Tyr Lys Tyr Gly Phe Gly					
		485		490		495
25	Ala Pro Ala Ile Asp Asp Val Ser Leu Thr Ile Thr Ala Gly Glu Lys					
		500		505		510
30	Ile Ala Leu Val Gly Ile Ser Gly Ser Gly Lys Ser Thr Leu Val Lys					
		515		520		525
	Leu Leu Val Asn Phe Phe Gln Pro Glu Ser Gly Thr Ile Ser Leu Gly					
		530		535		540
35	Gln Thr Pro Leu Ala Asn Leu Asp Lys His Glu Leu Arg Ala His Ile					
		545		550		555
	Asn Tyr Leu Pro Gln Glu Pro Phe Ile Phe Ser Gly Ser Ile Met Asp					
		565		570		575
40	Asn Leu Leu Leu Gly Ala Lys Pro Gly Thr Thr Gln Glu Asp Ile Ile					
		580		585		590
45	Arg Ala Val Glu Ile Ala Glu Ile Lys Asp Asp Ile Glu Lys Met Ser					
		595		600		605
	Gln Gly Phe Gly Thr Glu Leu Ala Glu Ser Gly Asn Ile Ser Gly Gly					
		610		615		620
50	Gln Lys Gln Arg Ile Ala Leu Ala Arg Ala Ile Leu Val Asp Ser Pro					
		625		630		635
	Val Leu Ile Leu Asp Glu Ser Thr Ser Asn Leu Asp Val Leu Thr Glu					

	645		650		655
	Lys Lys Ile Ile Asp Asn Leu Met Gln Leu Thr Glu Lys Thr Ile Ile				
	660		665		670
5	Phe Val Ala His Arg Leu Thr Ile Ser Gln Arg Val Asp Arg Ile Leu				
	675		680		685
10	Thr Met Gln Asn Gly Lys Ile Ile Glu Asp Gly Thr His Asn Thr Leu				
	690		695		700
	Leu Asn Ala Gly Gly Phe Tyr Ala Ser Leu Phe Asn His				
	705		710		715

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 457 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: lcaD
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met	Phe	Asp	Pro	Lys	Tyr	Leu	Glu	Ser	Gly	Glu	Phe	Tyr	Gln	Arg	Arg
1				5					10					15	
Tyr	Arg	Asn	Phe	Pro	Thr	Leu	Ile	Ile	Val	Pro	Ile	Phe	Leu	Leu	Val
		20					25					30			
Val	Phe	Ile	Ile	Leu	Phe	Ser	Leu	Phe	Ala	Lys	Arg	Glu	Ile	Val	Val
		35				40					45				
Lys	Ala	Ser	Gly	Glu	Ile	Ile	Pro	Ala	Lys	Val	Leu	Ser	Asp	Ile	Gln
	50				55					60					
Ser	Thr	Ser	Asn	Asn	Ala	Ile	Asp	Ser	Asn	Gln	Leu	Thr	Glu	Asn	Lys
65				70					75					80	
Val	Val	Lys	Lys	Gly	Asp	Thr	Leu	Val	Thr	Phe	Thr	Ser	Gly	Asn	Glu
			85				90						95		
Lys	Ile	Ser	Ser	Gln	Leu	Leu	Thr	Gln	Gln	Leu	Asn	Asn	Leu	Asn	Asp

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	100	105	110
	Arg Leu Lys Ser Leu Asp Thr Tyr Lys Gln Ser Ile Val Asn Gly Arg		
	115	120	125
5	Ser Glu Phe Gly Gly Thr Asp Gln Phe Gly Tyr Asp Ser Leu Phe Asn		
	130	135	140
10	Gly Tyr Met Ala Gln Val Asp Thr Leu Thr Ser Glu Phe Asn Gln Gln		
	145	150	155 160
	Ser Ser Asp Lys Gln Thr Ala Asp Gln Gln Ala Asn His Gln Ile Asp		
	165	170	175
15	Val Leu Lys Gln Gly Gln Ser Lys Asn Asn Gln Gln Leu Ala Asn Tyr		
	180	185	190
20	Gln Ala Ile Leu Thr Ser Ile Asn Ser Asn Thr Lys Pro Thr Asn Asn		
	195	200	205
	Pro Tyr Gln Ala Ile Tyr Asp Asn Tyr Ser Ala Gln Leu Lys Ser Ala		
	210	215	220
25	Gln Thr Thr Asp Asp Lys Asp Gln Val Lys Gln Thr Ala Leu Ser Asn		
	225	230	235 240
	Val Gln Gln Gln Ile Asp Gln Leu Gln Thr Thr Ser Ser Ser Tyr Asp		
	245	250	255
30	Ser Gln Ile Ala Gly Ile Thr Lys Ser Gly Pro Leu Ser Gln Ser Ser		
	260	265	270
	Thr Leu Asp Lys Ile Ala Asp Leu Lys Gln Gln Gln Leu Ala Ser Ala		
	275	280	285
35	Gln Lys Glu Ile Asn Asp Gln Gln Gln Ser Leu Asp Glu Leu Lys Ala		
	290	295	300
40	Lys Gln Ser Ser Ala Asn Glu Asp Tyr Gln Asp Thr Val Ile Lys Ala		
	305	310	315 320
	Pro Glu Asp Gly Ile Leu His Leu Ala Thr Asp Lys Thr Lys Ile Lys		
	325	330	335
45	Tyr Phe Pro Lys Gly Thr Thr Ile Ala Gln Ile Tyr Pro Lys Leu Thr		
	340	345	350
	Gln Lys Thr Ala Leu Asn Val Glu Tyr Tyr Val Pro Ala Ser Asn Ile		
	355	360	365
50	Ile Gly Leu Lys Gln Arg Gln Ala Ile Arg Phe Val Ala Asn Gln Asn		
	370	375	380
	Val Thr Lys Pro Leu Thr Leu Asn Gly Thr Ile Lys Ser Ile Ser Ser		

385					390					395					400
Ala	Pro	Ile	Ala	Ser 405	Lys	Glu	Gly	Ser	Phe 410	Tyr	Lys	Leu	Val	Ala 415	Thr
Ile	Gln	Ala	Ser 420	Lys	Ile	Asp	Arg	Glu 425	Gln	Ile	Lys	Tyr	Gly 430	Leu	Asn
Gly	Arg	Ile 435	Thr	Thr	Ile	Lys	Gly 440	Thr	Lys	Thr	Trp	Phe 445	Asn	Tyr	Tyr
Lys	Asp 450	Ile	Val	Leu	Gly	Glu 455	Asn	Asn							

15 (2) INFORMATION FOR SEQ ID NO:6:

- ```
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 35 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

ii) MOLECULE TYPE: peptide

iii) HYPOTHETICAL: NO

iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

vi) IMMEDIATE SOURCE:
 (B) CLONE: Divergicin N-terminal

ix) FEATURE:
 (A) NAME/KEY: Cleavage-site
 (B) LOCATION: 29..30
```

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

```
Met Lys Lys Gln Ile Leu Lys Gly Leu Val Ile Val Val Cys Leu Ser
1 5 10 15
Gly Ala Thr Phe Phe Ser Thr Pro Gln Gln Ala Ser Ala Ala Ala Pro
 20 25 30
Lys Ile Thr
 35
```

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 29 amino acids

(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide  
(iii) HYPOTHETICAL: NO  
(iv) ANTI-SENSE: NO  
(v) FRAGMENT TYPE: N-terminal

(vii) IMMEDIATE SOURCE:  
(B) CLONE: Divergicin N-terminal, cleaved

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Lys Lys Gln Ile Leu Lys Gly Leu Val Ile Val Val Cys Leu Ser  
1 5 10 15  
Gly Ala Thr Phe Phe Ser Thr Pro Gln Gln Ala Ser Ala  
20 25

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 30 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide  
(iii) HYPOTHETICAL: NO  
(iv) ANTI-SENSE: NO  
(v) FRAGMENT TYPE: N-terminal

(vii) IMMEDIATE SOURCE:  
(B) CLONE: leucocin A N-terminal

(ix) FEATURE:  
(A) NAME/KEY: Cleavage-site  
(B) LOCATION: 24..25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Met Asn Met Lys Pro Thr Glu Ser Tyr Glu Gln Leu Asp Asn Ser  
1 5 10 15

Ala Leu Glu Gln Val Val Gly Gly Lys Tyr Tyr Gly Asn Gly  
20 25 30

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(vii) IMMEDIATE SOURCE:  
(B) CLONE: leucocin A, cleaved

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Met Asn Met Lys Pro Thr Glu Ser Tyr Glu Gln Leu Asp Asn Ser  
1 5 10 15

Ala Leu Glu Gln Val Val Gly Gly  
20

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 27 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(vii) IMMEDIATE SOURCE:  
(B) CLONE: lactococcin A N-terminal

(ix) FEATURE:  
(A) NAME/KEY: Cleavage-site

(B) LOCATION: 21..22

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Lys Asn Gln Leu Asn Phe Asn Ile Val Ser Asp Glu Glu Leu Ser  
1 5 10 15

Glu Ala Asn Gly Gly Lys Leu Thr Phe Ile Gln  
20 25

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(vii) IMMEDIATE SOURCE:

(B) CLONE: lactococcin A, cleaved

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Lys Asn Gln Leu Asn Phe Asn Ile Val Ser Asp Glu Glu Leu Ser  
1 5 10 15

Glu Ala Asn Gly Gly  
20

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(vii) IMMEDIATE SOURCE:  
(B) CLONE: colicin V, N-terminal

(ix) FEATURE:  
(A) NAME/KEY: Cleavage-site  
(B) LOCATION: 15..16

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met Arg Thr Leu Thr Leu Asn Glu Leu Asp Ser Val Ser Gly Gly Ala  
1 5 10 15  
Ser Gly Arg Asp Ile  
20

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(vii) IMMEDIATE SOURCE:  
(B) CLONE: colicin V, cleaved

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met Arg Thr Leu Thr Leu Asn Glu Leu Asp Ser Val Ser Gly Gly  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 3475 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

5

(vii) IMMEDIATE SOURCE:  
(B) CLONE: pCD3.4

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

|    |                                                                   |      |
|----|-------------------------------------------------------------------|------|
|    | GATATCTTGG TATTACAAAC TAATTGGAGG TTGGTATATA TGAAAAAACA AATTTTAAAA | 60   |
|    | GGGTTGGTTA TAGTTGTTTG TTTATCTGGG GCAACATTTT TCTCAACACC ACAACAAGCT | 120  |
| 15 | TCTGCTGCTG CACCGAAAAT TACTCAAAAA CAAAAAATT GTGTTAATGG ACAATTAGGT  | 180  |
|    | GGAATGCTTG CTGGAGCTTT GGGTGGACCT GGCGGAGTTG TGTTAGGTGG TATAGGTGGT | 240  |
| 20 | GCAATAGCAG GAGGTGTTT TAATTAAATG AAAATAAAAT GGTACTGGGA ATCTCTGATT  | 300  |
|    | GAAACCTTAA TATTTATAAT TGTTCTTCTT GTATTTTTTT ATAGAAGTTC TGGTTTTTCT | 360  |
| 25 | TTAAAAAATT TAGTTTTAGG AAGTTTATTT TATTTGATAG CAATTGGTCT TTTAATTAT  | 420  |
|    | AAAAAGATAA ACAAATAGGC ACTATTTTAA AATTTACAAC TTTTGCATTT TAAGTATATT | 480  |
|    | GTTGTTATTA TTAAGGTGCG AGATGAGATA AGGTCTACAT GGACAGCACA AAACCCACCC | 540  |
| 30 | CTAATGCGAA TAGGGGTGGG TTTTTTTCGT TCGTTGCGAA TACGAACGTG TGGGTTAGAG | 600  |
|    | ACAATTGCG AGATTATCGT CTAATCATCT AACCAATGAT CCACTAGTAT TAATACTAGT  | 660  |
| 35 | CCCACAAAAA GTGGAGCAAT AACCAATGAG ATAAGGTTTT CCATAAACAG CACCCCCTTT | 720  |
|    | CAGGGGCAAG TTGCCACTTA CTAATATAGC ACAGCTCCTT TATTGTTCTT AGTCTAAATC | 780  |
|    | TGATAAATCT TTTCTTGTTT AAAAATATAG ACCACTTAAA AGCTTATAAC GGTACTAGAT | 840  |
| 40 | TTTTCAGATA CCCCAATTAC CTACTTAAAA CGTCTCTCTT TTTCGTTTTA AGATGTTTAA | 900  |
|    | AATTATTTTC TATGAATTAT ACACAAATGT GCTTAAATCG TCTTAAATCG TCTTAAATG  | 960  |
| 45 | TGGTCTGTGT TGAGAATACA ACGACTTTGT TTGGTCGTAC CTCTAAATCT GTTTGCTGTG | 1020 |
|    | AACGAGGGTA GCGAAGTGAA CTTTTTGTG CTAACGCTCT TGGTTTTGTC TTTTGATTTT  | 1080 |
|    | ATAAAATGTG GATGTAATCC ACTCCTTACT AGGGGTTTAA TCTTTATAAA ATAAAGGAGC | 1140 |
| 50 | TTGCGAATGC AAGGTGCCCT TTTTCTTTG TCTGACTACT AGGGACAAAT TATCTGAGTA  | 1200 |
|    | TGAACAAGAT TTTGTCTGTT CTTGCGCGTA TTTATTAATA TATATTTTAA GAGATATTTT | 1260 |
|    | AAGAGATATT TTAAACCTT TTTAGGGGTG AGCTCAGCCT TAGAGAGAGT AAGCATTGAA  | 1320 |

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|    |                                                                    |      |
|----|--------------------------------------------------------------------|------|
|    | GCATAGTACT AGGGACAAAT TATCTGACTA CTAGGGATAA ATTATCTGAC TACTAGGGAC  | 1380 |
|    | AAATTATCTG ACTACTAGGG ATAAATTATC TGACTACTAG GGACGCACTT TACTTTGTGT  | 1440 |
| 5  | ATCGTATCGT TTATAATCTT TATATGTGAG GGGAGGTCTG AAGGATTGGA AAAGAAAACG  | 1500 |
|    | AATTTAAAAA TTGCATATCA AAATGAATTG AATCTGGTTC CACTTAAAAA TTTCAATGCT  | 1560 |
| 10 | AAACAAATGG ATTTATTCTT TGCTTTGTGT GCCCGAATGA AAAATAAAGG GCTTAGAAAAG | 1620 |
|    | GTATCTTTTA CGTTTGAAGA ACTAAGAGAA CTAAGTGATT ACAAGATAAC TGCTATCGAA  | 1680 |
|    | CCGTTACGA ATGATTTAGA ACAATTATAC AAAAAATGT TAAACCTAAC ATACAGAACG    | 1740 |
| 15 | GAGACAGAAA CAAAAATCAG TTATTTCTGT TTATTTACTG GGTGTGTGAT TGATAAATCA  | 1800 |
|    | GAGCAAATTG TTGAAGTTAG TGTAACCCA GACTTAGAAC ATATCATTAA CGGTATCTCT   | 1860 |
| 20 | AGTGAGTTCA ATAAATTTGA GTTACTAGCA TTCACAAGTA TCCAGTCGAA ATATACGAAA  | 1920 |
|    | ACACTCTTTA GATTGCTTAT GCAGTTTCAA TCAACTGGGT TTTATGTGGT TAAAATTGAA  | 1980 |
|    | GATTTTCAGAG CACTTTTAGA CATTCCAAAA TCTTATCAAA TGACTGACAT AACCCAACGG | 2040 |
| 25 | ATATTGAAAC CTAGTTTAAT TGAGTTAAGT CAGTACTTTA ATGATTTAAA AGTTAATAAA  | 2100 |
|    | ATTAAAGCTC GAAAGGGTAA TAAATAGAC CGTTTAGAAT TCACTTTCTC CGGTCTAAAG   | 2160 |
| 30 | ACTGATTTAC CTAAAGTTCC ATTGCACGAC TGGACGAAAT AAAAAAGGA CCTCCCCCTC   | 2220 |
|    | ACATTTAAGC AAGTAGGAAC GTCCCTCGCA ATCCACGAAG ACTGCTGATT CATTTTAGCA  | 2280 |
|    | TATATTGTGC GGGACTTCTA AATAAATTAT ATTTGGAGGT CATTTTATG TCGAATAAGT   | 2340 |
| 35 | ACTTGAAAAA AAGAAAGCGT CAAGCTAAGC AGGTAGCTGA TTTGTACGAT TTAATTATTG  | 2400 |
|    | GGGTTGAACA TGCTGGCAGC TCGTTAATTG CGTTGTATGA GGAATTAAA CCCTCTCAAT   | 2460 |
| 40 | ATCGAATTTT TATTCTTTTG TCTTATTCTA GTTTTGAAAA TAAATTAAAC TTATACAACA  | 2520 |
|    | AAGCGATTTT AAGAACTGAA GTTTATTCTT TAGAAAAAAA ATTAACGAA AAAATAAATG   | 2580 |
|    | CTCAAATCAG AATTGCGCAA AAAAATAAAA AAGAAATTGC GGTAATTGAT TTCACAAAAC  | 2640 |
| 45 | AAAAAGAAAA ACTCAAAGA GAATTACTTA GTTTTGAAAA TGATAAAGAA ATGAAACTTA   | 2700 |
|    | TGGATTGCA ATTAACAACAA TTTCATGAAA ATAAAACGTT AGCTGATATT AATGATCAGT  | 2760 |
| 50 | TTTTTATGAC GGTACAAAAT AGTTTAATTT TGCTGCATAA AAAAGCACCT TTAACATTAA  | 2820 |
|    | AATTAATTTG TTTGAAAAAT TATATTCGCC TTTGCAAAAA TTATTTTCTA AAGAATATAT  | 2880 |
|    | TTTAATGTTT TTTGAAAAAA ATAGTAACAT GGGAACATGT TGCTCTGCTC GCAAAAGGAA  | 2940 |



AAATATTTAA ACTAATAAAA AACCGTCGGA GACCAGCCAA CCAATAGGTT GGCTTTAAGT 3000  
TTAAGCCTAC GTTGACAACT GTCAATGTAT AAGTGCGCCC TTTGGGTGTT TTATTTTTTG 3060  
5 TTTAACTATT ATTTTCTGCA TAGGTTTTTT ATTTTATTA ATTTGATTTT CAAGAAAGGG 3120  
ATGAACCTAA AATGATTTAT AAACAAAAA AGAAAGAAGA TGTTTTTTGA TTCCTAAAG 3180  
10 TTTTAACAAT TGCTGATTG AGTACGAGAT GGAAATGTC ACGTCAAGCT ATCCATAAAA 3240  
AAATTCAAGA AGATTTATTA TTCCTATGC CTGTTCAAAT TGTCTCAAAT GGAAAAATTA 3300  
AATTGTTTTT ATTTGTTGAT ATTGAAAAAT ACGAAAAAAA TCGTCCGTGG TTATTAGACA 3360  
15 TTAATTATCG AAATGAACGA CAACTTTGGA TTTACAAAAA TGGTTTTTTT AAATAGCAAG 3420  
TTAGTCAATT ACCTTATACC TTGTTGGATA TCTTTGATA AAAAAATAGT TGTAT 3475

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 228 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

- (B) CLONE: Divergicin structural gene

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..228

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

ATG AAA AAA CAA ATT TTA AAA GGG TTG GTT ATA GTT GTT TGT TTA TCT 48  
45 Met Lys Lys Gln Ile Leu Lys Gly Leu Val Ile Val Val Cys Leu Ser  
1 5 10 15  
GGG GCA ACA TTT TTC TCA ACA CCA CAA CAA GCT TCT GCT GCT GCA CCG 96  
50 Gly Ala Thr Phe Phe Ser Thr Pro Gln Gln Ala Ser Ala Ala Pro  
20 25 30  
AAA ATT ACT CAA AAA CAA AAA AAT TGT GTT AAT GGA CAA TTA GGT GGA 144  
Lys Ile Thr Gln Lys Gln Lys Asn Cys Val Asn Gly Gln Leu Gly Gly  
35 40 45

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ATG CTT GCT GGA GCT TTG GGT GGA CCT GGC GGA GTT GTG TTA GGT GGT 192  
Met Leu Ala Gly Ala Leu Gly Gly Pro Gly Gly Val Val Leu Gly Gly  
50 55 60

5 ATA GGT GGT GCA ATA GCA GGA GGT TGT TTT AAT TA 228  
Ile Gly Gly Ala Ile Ala Gly Gly Cys Phe Asn  
65 70 75

10 (2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 75 amino acids  
(B) TYPE: amino acid  
15 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

20 Met Lys Lys Gln Ile Leu Lys Gly Leu Val Ile Val Val Cys Leu Ser  
1 5 10 15

25 Gly Ala Thr Phe Phe Ser Thr Pro Gln Gln Ala Ser Ala Ala Ala Pro  
20 25 30

Lys Ile Thr Gln Lys Gln Lys Asn Cys Val Asn Gly Gln Leu Gly Gly  
35 40 45

30 Met Leu Ala Gly Ala Leu Gly Gly Pro Gly Gly Val Val Leu Gly Gly  
50 55 60

35 Ile Gly Gly Ala Ile Ala Gly Gly Cys Phe Asn  
65 70 75

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 171 base pairs  
(B) TYPE: nucleic acid  
40 (C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

45 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

50 (iv) ANTI-SENSE: NO

- (vii) IMMEDIATE SOURCE:  
(B) CLONE: Divergicin immunity genes

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..171

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

10 ATG AAA ATA AAA TGG TAC TGG GAA TCT CTG ATT GAA ACC TTA ATA TTT 48  
Met Lys Ile Lys Trp Tyr Trp Glu Ser Leu Ile Glu Thr Leu Ile Phe  
1 5 10 15  
15 ATA ATT GTT CTT CTT GTA TTT TTT TAT AGA AGT TCT GGT TTT TCT TTA 96  
Ile Ile Val Leu Leu Val Phe Phe Tyr Arg Ser Ser Gly Phe Ser Leu  
20 25 30  
15 AAA AAT TTA GTT TTA GGA AGT TTA TTT TAT TTG ATA GCA ATT GGT CTT 144  
Lys Asn Leu Val Leu Gly Ser Leu Phe Tyr Leu Ile Ala Ile Gly Leu  
35 40 45  
20 TTT AAT TAT AAA AAG ATA AAC AAA TA 171  
Phe Asn Tyr Lys Lys Ile Asn Lys  
50 55

25 (2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 56 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

40 Met Lys Ile Lys Trp Tyr Trp Glu Ser Leu Ile Glu Thr Leu Ile Phe  
1 5 10 15  
Ile Ile Val Leu Leu Val Phe Phe Tyr Arg Ser Ser Gly Phe Ser Leu  
20 25 30  
Lys Asn Leu Val Leu Gly Ser Leu Phe Tyr Leu Ile Ala Ile Gly Leu  
35 40 45  
45 Phe Asn Tyr Lys Lys Ile Asn Lys  
50 55

50 (2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 124 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

5 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

10 (vii) IMMEDIATE SOURCE:  
(B) CLONE: Divergicin signal sequence

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide

15 (B) LOCATION: 1..123

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..123

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

25 ATC TTG GTA TCA CAA ACT AAT TTG GAG GTT GGT ATA TAT GAA AAA ACA 48  
Ile Leu Val Ser Gln Thr Asn Leu Glu Val Gly Ile Tyr Glu Lys Thr  
1 5 10 15

30 AAT TTT AAA AGG GTT GGT TAT AGT TGT TTG TTT ATC TGG GGC AAC ATT 96  
Asn Phe Lys Arg Val Gly Tyr Ser Cys Leu Phe Ile Trp Gly Asn Ile  
20 25 30

35 TTT CTC AAC ACC ACA ACA AGC TTC TGC T 124  
Phe Leu Asn Thr Thr Thr Ser Phe Cys  
35 40

(2) INFORMATION FOR SEQ ID NO:20:

40 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 41 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

45 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

50 Ile Leu Val Ser Gln Thr Asn Leu Glu Val Gly Ile Tyr Glu Lys Thr  
1 5 10 15

Asn Phe Lys Arg Val Gly Tyr Ser Cys Leu Phe Ile Trp Gly Asn Ile  
20 25 30

Phe Leu Asn Thr Thr Thr Ser Phe Cys

35

40

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 675 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:  
(B) CLONE: Brochocin-C

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

|             |             |             |            |            |            |     |
|-------------|-------------|-------------|------------|------------|------------|-----|
| GCTATTTTGA  | GAAATATTAA  | CCAATAGTAA  | AAATTATCAT | GCTATCTTTT | GTATGTAATA | 60  |
| AAAATTATTT  | AAAGGAGGGT  | GTTTCATCAT  | GCACAAGGTA | AAAAAATTAA | ACAATCAAGA | 120 |
| GTTACAACAG  | ATCGTGGGAG  | GTTACAGTTC  | AAAAGATTGT | CTAAAAGATA | TTGGTAAAGG | 180 |
| AATTGGTGCT  | GGTACAGTAG  | CTGGGGCAGC  | CGGCGGTGGC | CTAGCTGCAG | GATTAGGTGC | 240 |
| TATCCCAGGA  | GCATTCGTTG  | GAGCACATTT  | TGGAGTAATC | GGCGGATCTG | CCGCATGCAT | 300 |
| TGGTGGATTA  | TTAGGTA ACT | AGGAGGTTAT  | ATTTATGAAA | AAAGAACTAT | TGAATAAAAA | 360 |
| TGAAATGAGT  | AGAATTATCG  | GCGGC AAAAT | AAATTGGGGA | AATGTTGGCG | GTTCTTGTGT | 420 |
| TGGAGGTGCA  | GTAATTGGAG  | GCGCCCTCGG  | TGGACTAGGT | GGAGCTGGCG | GAGGTTGCAT | 480 |
| TACAGGAGCT  | ATCGGAAGTA  | TTTGGGATCA  | ATGGTAAAAA | CTATACTATT | TTCGGTTGTA | 540 |
| ATTCATTTCG  | TTGCATTATG  | TAAC TTTTTA | ATAAAAAAAG | ATGTGTCTTC | AAAAAAAAAA | 600 |
| TTATTTT TAA | CAGGTTCTAT  | TGCTGTCTTT  | CTAATTATCT | ATGATTTTCT | ATGGATTATA | 660 |
| TTCTCTAACT  | AGTAC       |             |            |            |            | 675 |

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 234 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

5 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

10 (vii) IMMEDIATE SOURCE:

(B) CLONE: Brochocin-C peptide A

(ix) FEATURE:

(A) NAME/KEY: CDS

15 (B) LOCATION: 1..234

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide

(B) LOCATION: 1..54

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

20  
25 ATG CAC AAG GTA AAA AAA TTA AAC AAT CAA GAG TTA CAA CAG ATC GTG 48  
Met His Lys Val Lys Lys Leu Asn Asn Gln Glu Leu Gln Gln Ile Val  
1 5 10 15

30 GGA GGT TAC AGT TCA AAA GAT TGT CTA AAA GAT ATT GGT AAA GGA ATT 96  
Gly Gly Tyr Ser Ser Lys Asp Cys Leu Lys Asp Ile Gly Lys Gly Ile  
20 25 30

35 GGT GCT GGT ACA GTA GCT GGG GCA GCC GGC GGT GGC CTA GCT GCA GGA 144  
Gly Ala Gly Thr Val Ala Gly Ala Ala Gly Gly Gly Leu Ala Ala Gly  
35 40 45

40 TTA GGT GCT ATC CCA GGA GCA TTC GTT GGA GCA CAT TTT GGA GTA ATC 192  
Leu Gly Ala Ile Pro Gly Ala Phe Val Gly Ala His Phe Gly Val Ile  
50 55 60

45 GGC GGA TCT GCC GCA TGC ATT GGT GGA TTA TTA GGT AAC TA 234  
Gly Gly Ser Ala Ala Cys Ile Gly Gly Leu Leu Gly Asn  
65 70 75

50 (2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 77 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Met His Lys Val Lys Lys Leu Asn Asn Gln Glu Leu Gln Gln Ile Val  
1 5 10 15  
5 Gly Gly Tyr Ser Ser Lys Asp Cys Leu Lys Asp Ile Gly Lys Gly Ile  
20 25 30  
Gly Ala Gly Thr Val Ala Gly Ala Ala Gly Gly Gly Leu Ala Ala Gly  
35 40 45  
10 Leu Gly Ala Ile Pro Gly Ala Phe Val Gly Ala His Phe Gly Val Ile  
50 55 60  
Gly Gly Ser Ala Ala Cys Ile Gly Gly Leu Leu Gly Asn  
65 70 75  
15

(2) INFORMATION FOR SEQ ID NO:24:

- 20 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 183 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
25 (ii) MOLECULE TYPE: DNA (genomic)  
(iii) HYPOTHETICAL: NO  
(iv) ANTI-SENSE: NO  
30 (vii) IMMEDIATE SOURCE:  
(B) CLONE: Brochocin-C peptide B  
35 (ix) FEATURE:  
(A) NAME/KEY: CDS  
(B) LOCATION: 1..183  
40 (ix) FEATURE:  
(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 1..51  
45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| ATG AAA AAA GAA CTA TTG AAT AAA AAT GAA ATG AGT AGA ATT ATC GGC    | 48  |
| Met Lys Lys Glu Leu Leu Asn Lys Asn Glu Met Ser Arg Ile Ile Gly    |     |
| 1 5 10 15                                                          |     |
| 50 GGC AAA ATA AAT TGG GGA AAT GTT GGC GGT TCT TGT GTT GGA GGT GCA | 96  |
| Gly Lys Ile Asn Trp Gly Asn Val Gly Gly Ser Cys Val Gly Gly Ala    |     |
| 20 25 30                                                           |     |
| GTA ATT GGA GGC GCC CTC GGT GGA CTA GGT GGA GCT GGC GGA GGT TGC    | 144 |

Val Ile Gly Gly Ala Leu Gly Gly Leu Gly Gly Ala Gly Gly Gly Cys  
35 40 45

5 ATT ACA GGA GCT ATC GGA AGT ATT TGG GAT CAA TGG TA  
Ile Thr Gly Ala Ile Gly Ser Ile Trp Asp Gln Trp  
50 55 60

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(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 60 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

20 Met Lys Lys Glu Leu Leu Asn Lys Asn Glu Met Ser Arg Ile Ile Gly  
1 5 10 15  
Gly Lys Ile Asn Trp Gly Asn Val Gly Gly Ser Cys Val Gly Gly Ala  
20 25 30  
25 Val Ile Gly Gly Ala Leu Gly Gly Leu Gly Gly Ala Gly Gly Gly Cys  
35 40 45  
30 Ile Thr Gly Ala Ile Gly Ser Ile Trp Asp Gln Trp  
50 55 60

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 162 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: Brochocin-C immunity peptide

(ix) FEATURE:

- (A) NAME/KEY: CDS  
(B) LOCATION: 1..162



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

[illegible]

20 (2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

30 Met Val Lys Thr Ile Leu Phe Ser Val Val Ile Ser Phe Val Ala Leu  
1 5 10 15

35 Cys Asn Phe Leu Ile Lys Lys Asp Val Ser Ser Lys Lys Lys Leu Phe  
20 25 30

Leu Thr Gly Ser Ile Ala Val Phe Leu Ile Ile Tyr Asp Phe Leu Trp  
35 40 45

40 Ile Ile Phe Ser Asn  
50

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2226 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

5 (B) CLONE: Enterocin 900 operon

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

10 AAGCTTTACT TGATATTAGT TCTGAGTTCT GCCTGATTTA TCAGTAACAT AACTCTAGAG 60  
ATAACTGCGT CGCTATCTCA AGTTCTTTTT TCTTTTCTTA CAAAATAAAT ATACTTTATT 120  
TCATTTTATA AGTCAACGTT TTCATTGCTT ATAAATTAGT TTTTAAATC ATCTCAGTAA 180  
15 TAATTTGCTA TGTCAGTTCG ATCAATACCA TTTGCATGAA AGTACAGCTA TAAGCCAATC 240  
ACACCTAACC TACTCTTAAT CGTATAATGA TTCCAGTTAG CAAGGTCTTT AATACTCATG 300  
20 ATCCCCATCT GGTGAGTTT TTTTCATTCG AAACCCTATG CCCCAAAAGA CCGTCATTTT 360  
AGGAATATTC CATACTTTCT CAGGAACATT TTGATACGTC CATTACAGCA TAAACCCTTC 420  
ATTGTGCTTC GCTTCATTGT CTAAGGCGAG TTTGGCCAAA GGGGATTATC TCCGCGACAC 480  
25 CTACCGTAGC AATCAATCCT AATTCTTCTT TAATACGTTT CTTGGATCAT TTGAACGAAT 540  
TTTTTCCTTC TCTGACTTCT TGTTCTTCA GTCGTAAAAA TATTCAGTGA TCTGGTCACT 600  
30 TTTAAATGG GTTCATCGAT TGGATACATC AGTAGATCTT CGTCAGCCAC ATATCTTTTG 660  
AAAATATTAT TTACCCGCAT ATTCGCTTG ATATATAGGT TCATACGTGG TGGAACAACG 720  
TATGATGTTT TAGGAAATAG TTGTGATAAA TCACGTGGTC TACTCACATT TGTAATATCA 780  
35 TACCGCTTTT TTGCTTCAGG AGAAGAAGCT CTAATATCAA TCCTAAACCA GTATTGTCAG 840  
CGCGACTCAT AACAACAAGT TCTGTTGTTA ATGGATCAAA ATTTCTTTCT ATACACTCGA 900  
40 TACTCGCATA AAAAGGCTTC ATGTCGATTA GAAAATAATC ATTTACTGAT TCTTTTGAAT 960  
AATCCAGCAT GAATAACACC CATTCTTTTT CACATTACAC AAACGTAAGT TAGGAAATAT 1020  
AAAGAAGAAA ACTAAATAGC ACTAAACAAA CAAGACAACT CATGCTTATT CCGTATAAGA 1080  
45 AACTACATAT TATGTAACT AGTTATTAAA ATAACATATT TAATAAAATT AAATTGTGAT 1140  
TTTATAGGTT TCAGGAATGA AAAAGCCTTA TTTCAGGAAG TTTTAACTG TTTGCTATAG 1200  
50 ATGTATGTCA TGATAGCATC GTAATAAAAA TACTCTAAAA GGAGCGAGTT TAAATATGCA 1260  
AAATGTAAAA GAATTAAGTA CGAAAGAGAT GAAACAAATT ATCGGTGGAG AAAATGATCA 1320  
CAGAATGCCT AATGAGTTAA ATAGACCTAA CAACTTATCT AAAGGTGGAG CAAAATGTGG 1380

TGCTGCAATT GCTGGGGGAT TATTTGGAAT CCCAAAAGGA CCACTAGCAT GGGCTGCTGG 1440  
GTTAGCAAAT GTATACTCTA AATGCAACTA AAAAAGAAGA GAAAAAACTC ATTACGAGTT 1500  
5 TTTTCTCTTC TTTTTTTGCA TGAAATTAGG AATAACTAAT AAAACAATAG CAATCAATAG 1560  
TAAATCTTA CTTAATATAG TTTCGGAAAA AATAAATAAT CCTAAATTTA TAATTACTGC 1620  
10 TAAAAAATG CATAAATTAT ACTCTAAATT ATTTTTTTTTT AAATTCATAA TATAACATC 1680  
CTCTCTTTAA TTAGTCTACC ATTCCGAAAT ATTCATCCC CAGCTCTTTT TTTACTAATA 1740  
TACCAACTAC ATTTAATAAC AAAATAACTA GTAAACTTAA TATTTT TAGT GGCATAGAAT 1800  
15 ATTCAAAAAT AAATAAAGGC ACCATACATG TAGCTATCAA TATAAATACA GAACTTACGT 1860  
ATTTTATTAT TTTACGGAAC ATTATAACCT ATTACAAC TC CGCAAATAGC CATAGCCCAT 1920  
ACCATAGATA AGATTTTTTAC CAGCACCACC ACCACATGTT TGTTTTATCT CTTTCATACT 1980  
20 TAATTTTTTTT ACATTTTGCA TGTCTCTACA TGCTCCTTTT AAAGTTTTTTT TAGAACCTCA 2040  
CGACTATAAC ATGGATAATT TAATCGTGGT CAAAAACTTC CTGAAATAGG GTGTTTCATA 2100  
25 TCCTGAACAC GAATTTTTTAG TCAATTTTCG AAAAATGAAA CTTTAAAATT TCTTTGACCA 2160  
GAACTCTATT TATTCTTG TGTTTCCTTC GAATAGGTTC CCGTATATCT TTTTATTG 2220  
AAGCTT 2226

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: Enterocin 900 peptide

(ix) FEATURE:

- (A) NAME/KEY: CDS  
(B) LOCATION: 1..216

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide

(B) LOCATION: 1..54

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

5  
ATG CAA AAT GTA AAA GAA TTA AGT ACG AAA GAG ATG AAA CAA ATT ATC 48  
Met Gln Asn Val Lys Glu Leu Ser Thr Lys Glu Met Lys Gln Ile Ile  
1 5 10 15  
10 GGT GGA GAA AAT GAT CAC AGA ATG CCT AAT GAG TTA AAT AGA CCT AAC 96  
Gly Gly Glu Asn Asp His Arg Met Pro Asn Glu Leu Asn Arg Pro Asn  
20 25 30  
15 AAC TTA TCT AAA GGT GGA GCA AAA TGT GGT GCT GCA ATT GCT GGG GGA 144  
Asn Leu Ser Lys Gly Gly Ala Lys Cys Gly Ala Ala Ile Ala Gly Gly  
35 40 45  
TTA TTT GGA ATC CCA AAA GGA CCA CTA GCA TGG GCT GCT GGG TTA GCA 192  
Leu Phe Gly Ile Pro Lys Gly Pro Leu Ala Trp Ala Ala Gly Leu Ala  
50 55 60  
AAT GTA TAC TCT AAA TGC AAC TA 216  
Asn Val Tyr Ser Lys Cys Asn  
65 70

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Met Gln Asn Val Lys Glu Leu Ser Thr Lys Glu Met Lys Gln Ile Ile  
1 5 10 15  
40 Gly Gly Glu Asn Asp His Arg Met Pro Asn Glu Leu Asn Arg Pro Asn  
20 25 30  
45 Asn Leu Ser Lys Gly Gly Ala Lys Cys Gly Ala Ala Ile Ala Gly Gly  
35 40 45  
Leu Phe Gly Ile Pro Lys Gly Pro Leu Ala Trp Ala Ala Gly Leu Ala  
50 55 60  
50 Asn Val Tyr Ser Lys Cys Asn  
65 70

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 103 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: Colicin V prepeptide

(ix) FEATURE:

(A) NAME/KEY: Disulfide-bond

(B) LOCATION: 91..102

(ix) FEATURE:

(A) NAME/KEY: Cleavage-site

(B) LOCATION: 15..16

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Arg | Thr | Leu | Thr | Leu | Asn | Glu | Leu | Asp | Ser | Val | Ser | Gly | Gly | Ala |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Gly | Arg | Asp | Ile | Ala | Met | Ala | Ile | Gly | Thr | Leu | Ser | Gly | Gln | Phe |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Val | Ala | Gly | Gly | Ile | Gly | Ala | Ala | Ala | Gly | Gly | Val | Ala | Gly | Gly | Ala |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |
| Ile | Tyr | Asp | Tyr | Ala | Ser | Thr | His | Lys | Pro | Asn | Pro | Ala | Met | Ser | Pro |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Ser | Gly | Leu | Gly | Gly | Thr | Ile | Lys | Gln | Lys | Pro | Glu | Gly | Ile | Pro | Ser |
|     |     |     | 65  |     |     | 70  |     |     |     | 75  |     |     |     | 80  |     |
| Glu | Ala | Trp | Asn | Tyr | Ala | Ala | Gly | Arg | Leu | Cys | Asn | Trp | Ser | Pro | Asn |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Asn | Leu | Ser | Asp | Val | Cys | Leu |     |     |     |     |     |     |     |     |     |
|     |     |     |     |     |     | 100 |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 88 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:  
(B) CLONE: Colicin V

(ix) FEATURE:  
(A) NAME/KEY: Disulfide-bond  
(B) LOCATION: 76..87

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Ser | Gly | Arg | Asp | Ile | Ala | Met | Ala | Ile | Gly | Thr | Leu | Ser | Gly | Gln |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Phe | Val | Ala | Gly | Gly | Ile | Gly | Ala | Ala | Ala | Gly | Gly | Val | Ala | Gly | Gly |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |     |
| Ala | Ile | Tyr | Asp | Tyr | Ala | Ser | Thr | His | Lys | Pro | Asn | Pro | Ala | Met | Ser |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     |     | 45  |     |     |
| Pro | Ser | Gly | Leu | Gly | Gly | Thr | Ile | Lys | Gln | Lys | Pro | Glu | Gly | Ile | Pro |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ser | Glu | Ala | Trp | Asn | Tyr | Ala | Ala | Gly | Arg | Leu | Cys | Asn | Trp | Ser | Pro |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Asn | Asn | Leu | Ser | Asp | Val | Cys | Leu |     |     |     |     |     |     |     |     |
|     |     |     |     | 85  |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 675 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:  
(B) CLONE: carnobacteriocin BM1

(ix) FEATURE:  
 (A) NAME/KEY: RBS  
 (B) LOCATION: 89..93

5 (ix) FEATURE:  
 (A) NAME/KEY: RBS  
 (B) LOCATION: 290..293

10 (ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 103..285

15 (ix) FEATURE:  
 (A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 103..150

(ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 303..566

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| TCGAGATACG TTTATCCATG GTTCAGGATG ATTTTATCAA CGAGTTAATT ATTTATGCTA | 60  |
| CAGTAAACTT GTTACTAAAT ACTTTATAAG GAGTGTATGT AC ATG AAA AGC GTT    | 114 |
| Met Lys Ser Val                                                   |     |
| 1                                                                 |     |
| AAA GAA CTA AAT AAA AAA GAA ATG CAA CAA ATT AAT GGT GGA GCT ATC   | 162 |
| Lys Glu Leu Asn Lys Lys Glu Met Gln Gln Ile Asn Gly Gly Ala Ile   |     |
| 5 10 15 20                                                        |     |
| TCT TAT GGC AAT GGT GTT TAT TGT AAC AAA GAG AAA TGT TGG GTA AAC   | 210 |
| Ser Tyr Gly Asn Gly Val Tyr Cys Asn Lys Glu Lys Cys Trp Val Asn   |     |
| 25 30 35                                                          |     |
| AAG GCA GAA AAC AAA CAA GCT ATT ACT GGA ATA GTT ATC GGT GGA TGG   | 258 |
| Lys Ala Glu Asn Lys Gln Ala Ile Thr Gly Ile Val Ile Gly Gly Trp   |     |
| 40 45 50                                                          |     |
| GCT TCT AGT TTA GCA GGA ATG GGA CAT TAAAGAGGTA TCTAGTT ATG ATA    | 308 |
| Ala Ser Ser Leu Ala Gly Met Gly His                               |     |
| 55 60 1                                                           |     |
| Met Ile                                                           |     |
| AAA GAT GAA AAA ATA AAT AAA ATC TAT GCT TTA GTT AAG AGC GCA CTT   | 356 |
| Lys Asp Glu Lys Ile Asn Lys Ile Tyr Ala Leu Val Lys Ser Ala Leu   |     |
| 5 10 15                                                           |     |
| GAT AAT ACG GAT GTT AAG AAT GAT AAA AAA CTT TCT TTA CTT CTT ATG   | 404 |
| Asp Asn Thr Asp Val Lys Asn Asp Lys Lys Leu Ser Leu Leu Leu Met   |     |
| 20 25 30                                                          |     |
| AGA ATA CAA GAA ACA TCA ATT AAT GGA GAA CTA TTT TAC GAT TAT AAA   | 452 |

Arg Ile Gln Glu Thr Ser Ile Asn Gly Glu Leu Phe Tyr Asp Tyr Lys  
35 40 45 50

5 AAA GAA TTA CAG CCA GCT ATT AGT ATG TAC TCT ATT CAA CAT AAC TTT 500  
Lys Glu Leu Gln Pro Ala Ile Ser Met Tyr Ser Ile Gln His Asn Phe  
55 60 65

10 CGG GTT CCT GAC GAT CTA GTA AAA CTG TTA GCA TTA GTT CAA ACA CCT 548  
Arg Val Pro Asp Asp Leu Val Lys Leu Leu Ala Leu Val Gln Thr Pro  
70 75 80

15 AAA GCT TGG TCA GGG TTT TAACTTTAGT TCCAGATGAG TTAAATCCT 596  
Lys Ala Trp Ser Gly Phe  
85

TAAAAATAAG GAATAATGGT AAATCAGCAT TCCTTATTTT TATAGTCATC ACACTATAAC 656

TTTACTTAAA GATGTTCTGA 675

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 61 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Met Lys Ser Val Lys Glu Leu Asn Lys Lys Glu Met Gln Gln Ile Asn  
1 5 10 15

35 Gly Gly Ala Ile Ser Tyr Gly Asn Gly Val Tyr Cys Asn Lys Glu Lys  
20 25 30

40 Cys Trp Val Asn Lys Ala Glu Asn Lys Gln Ala Ile Thr Gly Ile Val  
35 40 45

Ile Gly Gly Trp Ala Ser Ser Leu Ala Gly Met Gly His  
50 55 60

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 88 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:



Met Ile Lys Asp Glu Lys Ile Asn Lys Ile Tyr Ala Leu Val Lys Ser  
1 5 10 15

5 Ala Leu Asp Asn Thr Asp Val Lys Asn Asp Lys Lys Leu Ser Leu Leu  
20 25 30

Leu Met Arg Ile Gln Glu Thr Ser Ile Asn Gly Glu Leu Phe Tyr Asp  
35 40 45

10 Tyr Lys Lys Glu Leu Gln Pro Ala Ile Ser Met Tyr Ser Ile Gln His  
50 55 60

Asn Phe Arg Val Pro Asp Asp Leu Val Lys Leu Leu Ala Leu Val Gln  
65 70 75 80

15 Thr Pro Lys Ala Trp Ser Gly Phe  
85

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1907 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

- (B) CLONE: carnobacteriocin B2 operon

(ix) FEATURE:

- (A) NAME/KEY: -35\_signal
- (B) LOCATION: 165..170

(ix) FEATURE:

- (A) NAME/KEY: -10\_signal
- (B) LOCATION: 189..193

(ix) FEATURE:

- (A) NAME/KEY: RBS
- (B) LOCATION: 221..225

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 236..433

(ix) FEATURE:

- (A) NAME/KEY: RBS

(B) LOCATION: 460..465

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 473..805

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1025..1267

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

|    |                                                                   |     |
|----|-------------------------------------------------------------------|-----|
| 15 | AAGCTTTTAT AGTACAATTA TTTATGCGTG CTATGCAATA GCTATTGTAT ATACTATTTT | 60  |
|    | TACTATGAGA AAAGATTCTT ATGAAAATAA CAAAAATAAT CGTAAAAAAG TTATATAGCA | 120 |
|    | TTTATTTTCAT TTATGAATTC AAATACCCTG GTTCAAGATG TATTTTCCAA AAAAATGTC | 180 |
| 20 | AGATATGATA TAGTTTTTTTT GAAATACAAA TATAAAATAA AGGAGTTTGA TTTAG ATG | 238 |
|    | Met                                                               |     |
|    | 1                                                                 |     |
| 25 | AAT AGC GTA AAA GAA TTA AAC GTG AAA GAA ATG AAA CAA TTA CAC GGT   | 286 |
|    | Asn Ser Val Lys Glu Leu Asn Val Lys Glu Met Lys Gln Leu His Gly   |     |
|    | 5 10 15                                                           |     |
| 30 | GGA GTA AAT TAT GGT AAT GGT GTT TCT TGC AGT AAA ACA AAA TGT TCA   | 334 |
|    | Gly Val Asn Tyr Gly Asn Gly Val Ser Cys Ser Lys Thr Lys Cys Ser   |     |
|    | 20 25 30                                                          |     |
| 35 | GTT AAC TGG GGA CAA GCC TTT CAA GAA AGA TAC ACA GCT GGA ATT AAC   | 382 |
|    | Val Asn Trp Gly Gln Ala Phe Gln Glu Arg Tyr Thr Ala Gly Ile Asn   |     |
|    | 35 40 45                                                          |     |
| 40 | TCA TTT GTA AGT GGA GTC GCT TCT GGG GCA GGA TCC ATT GGT AGG AGA   | 430 |
|    | Ser Phe Val Ser Gly Val Ala Ser Gly Ala Gly Ser Ile Gly Arg Arg   |     |
|    | 50 55 60 65                                                       |     |
| 45 | CCG TAAATATATA AATACAATAT AGAGCAAGGT GGTGATACA ATG GAT ATA AAG    | 484 |
|    | Pro Met Asp Ile Lys                                               |     |
|    | 1                                                                 |     |
| 50 | TCT CAA ACA TTA TAT TTG AAT CTA AGC GAG GCA TAT AAA GAC CCT GAA   | 532 |
|    | Ser Gln Thr Leu Tyr Leu Asn Leu Ser Glu Ala Tyr Lys Asp Pro Glu   |     |
|    | 5 10 15 20                                                        |     |
|    | GTA AAA GCT AAT GAA TTC TTA TCA AAA TTA GTT GTA CAA TGT GCT GGG   | 580 |
|    | Val Lys Ala Asn Glu Phe Leu Ser Lys Leu Val Val Gln Cys Ala Gly   |     |
|    | 25 30 35                                                          |     |
|    | AAA TTA ACA GCT TCA AAC AGT GAG AAC AGT TAT ATT GAA GTA ATA TCA   | 628 |
|    | Lys Leu Thr Ala Ser Asn Ser Glu Asn Ser Tyr Ile Glu Val Ile Ser   |     |
|    | 40 45 50                                                          |     |

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|    |                                                                   |      |
|----|-------------------------------------------------------------------|------|
|    | TTG CTA TCT AGG GGT ATT TCT AGT TAT TAT TTA TCC CAT AAA CGT ATA   | 676  |
|    | Leu Leu Ser Arg Gly Ile Ser Ser Tyr Tyr Leu Ser His Lys Arg Ile   |      |
|    | 55 60 65                                                          |      |
| 5  | ATT CCT TCA AGT ATG TTA ACT ATA TAT ACT CAA ATA CAA AAG GAT ATA   | 724  |
|    | Ile Pro Ser Ser Met Leu Thr Ile Tyr Thr Gln Ile Gln Lys Asp Ile   |      |
|    | 70 75 80                                                          |      |
| 10 | AAA AAC GGG AAT ATT GAC ACC GAA AAA TTA AGG AAA TAT GAG ATA GCA   | 772  |
|    | Lys Asn Gly Asn Ile Asp Thr Glu Lys Leu Arg Lys Tyr Glu Ile Ala   |      |
|    | 85 90 95 100                                                      |      |
| 15 | AAA GGA TTA ATG TCC GTT CCT TAT ATA TAT TTC TAATTTTTTC AATGATGTTA | 825  |
|    | Lys Gly Leu Met Ser Val Pro Tyr Ile Tyr Phe                       |      |
|    | 105 110                                                           |      |
|    | GTTGACTTCA AAAAGATGTG AAATCGATTA GCATTTTCAA AATTAGATTA AAAATACTAT | 885  |
| 20 | CTATATAAAA TAGAACTACT GATTTAAAGT ATTTATAAGA ATATAAAGTA GCAAATAACA | 945  |
|    | TGATAGACAC AATTAAGGAG CGACATTTTA TGGAAAATTT GAAATGGTAT TCGGGCGGGA | 1005 |
| 25 | ACGATAGAAA AAAAAAGCA ATG GCT ACT ATT ACT GAT TTG TTA AAC GAT TTA  | 1057 |
|    | Met Ala Thr Ile Thr Asp Leu Leu Asn Asp Leu                       |      |
|    | 1 5 10                                                            |      |
| 30 | AAA ATA GAC TTA GGT AAC GAA TCT CTA CAA AAT GTC TTA GAA AAT TAT   | 1105 |
|    | Lys Ile Asp Leu Gly Asn Glu Ser Leu Gln Asn Val Leu Glu Asn Tyr   |      |
|    | 15 20 25                                                          |      |
| 35 | CTT GAA GAA TTG GAA CAA GCA AAT GCT GCT GTT CCA ATT ATA TTA GGC   | 1153 |
|    | Leu Glu Glu Leu Glu Gln Ala Asn Ala Ala Val Pro Ile Ile Leu Gly   |      |
|    | 30 35 40                                                          |      |
| 40 | CGT ATG AAC ATA GAT ATC TCT ACA GCA ATC AGA AAA GAT GGT GTT ACT   | 1201 |
|    | Arg Met Asn Ile Asp Ile Ser Thr Ala Ile Arg Lys Asp Gly Val Thr   |      |
|    | 45 50 55                                                          |      |
| 45 | TTA TCA GAA ATT CAG TCT AAA AAA TTA AAA GAG CTG ATT TCA ATA TCC   | 1249 |
|    | Leu Ser Glu Ile Gln Ser Lys Lys Leu Lys Glu Leu Ile Ser Ile Ser   |      |
|    | 60 65 70 75                                                       |      |
| 50 | TAT ATT AAA TAT GGC TAT TAATTTAGTA TTAATAACAG TGTAGGATTG          | 1297 |
|    | Tyr Ile Lys Tyr Gly Tyr                                           |      |
|    | 80                                                                |      |
|    | ATTCAAATTA TTTGAATCAA AATTTATATA CAAATTTTAT TTATTTTGGG TCTTTAAATA | 1357 |
|    | ATTTTGTGTA AGTTCAAATT ATTTAAAGAT GAGTTAAAC TCTATCTTCG AAAACATCA   | 1417 |
|    | CAAAATGTGA TGAAATTTGT CCCCAATTTT GGACCTTCAT GGTCCATTTT TTCGTTACAT | 1477 |
|    | CCATCGTCAC TAAACAAAGC ATTTTtagta AGGATTCATC AGATGGGAAT ACTACCTTAG | 1537 |

ATTTTGTGG CTTTCACAGC TGACAATGGA GGCCTTCAAT CACATTGGCG GTATAAATAA 1597  
TCCGGCGCAA ATCTGCTGAA TACTTGAAAA ATGTCGCTAA TTCTGCCCAG TTATCTATCA 1657  
5 ATTCTTCAAT TAATTTGTCT GCGTTTATAT CCATTTTCAT TCCCCTTTTT TAATTTTCA 1717  
TTTTTTAGTT ACTTTAAACG GTTTAAAGCC TTAAGCACTT AGGCTTTAAT CTTTTTTCAC 1777  
10 TTGATCTAAT TATTTGAACT TCAGCATTGA TCTTTTGATT TATTCTTTTA GGAATTGAC 1837  
CGAATAGGGA GATTTCCTGT GAGTAGGCGC CAACGGTGGT GCGGTCGGA GTCAGCCGAC 1897  
TCACAAGCTT 1907

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Met Asn Ser Val Lys Glu Leu Asn Val Lys Glu Met Lys Gln Leu His  
1 5 10 15  
Gly Gly Val Asn Tyr Gly Asn Gly Val Ser Cys Ser Lys Thr Lys Cys  
20 25 30  
Ser Val Asn Trp Gly Gln Ala Phe Gln Glu Arg Tyr Thr Ala Gly Ile  
35 40 45  
Asn Ser Phe Val Ser Gly Val Ala Ser Gly Ala Gly Ser Ile Gly Arg  
50 55 60  
Arg Pro  
65

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Met Asp Ile Lys Ser Gln Thr Leu Tyr Leu Asn Leu Ser Glu Ala Tyr

1 5 10 15  
Lys Asp Pro Glu Val Lys Ala Asn Glu Phe Leu Ser Lys Leu Val Val  
20 25 30  
5 Gln Cys Ala Gly Lys Leu Thr Ala Ser Asn Ser Glu Asn Ser Tyr Ile  
35 40 45  
10 Glu Val Ile Ser Leu Leu Ser Arg Gly Ile Ser Ser Tyr Tyr Leu Ser  
50 55 60  
His Lys Arg Ile Ile Pro Ser Ser Met Leu Thr Ile Tyr Thr Gln Ile  
65 70 75 80  
15 Gln Lys Asp Ile Lys Asn Gly Asn Ile Asp Thr Glu Lys Leu Arg Lys  
85 90 95  
Tyr Glu Ile Ala Lys Gly Leu Met Ser Val Pro Tyr Ile Tyr Phe  
100 105 110

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Met Ala Thr Ile Thr Asp Leu Leu Asn Asp Leu Lys Ile Asp Leu Gly  
1 5 10 15  
35 Asn Glu Ser Leu Gln Asn Val Leu Glu Asn Tyr Leu Glu Glu Leu Glu  
20 25 30  
40 Gln Ala Asn Ala Ala Val Pro Ile Ile Leu Gly Arg Met Asn Ile Asp  
35 40 45  
Ile Ser Thr Ala Ile Arg Lys Asp Gly Val Thr Leu Ser Glu Ile Gln  
50 55 60  
45 Ser Lys Lys Leu Lys Glu Leu Ile Ser Ile Ser Tyr Ile Lys Tyr Gly  
65 70 75 80  
Tyr

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:  
10 (B) CLONE: JMc7

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

15 CCCAAGCTTC TGCTGTAAAT TATGGTAATG GTGTT

35

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:  
20 (A) LENGTH: 36 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:  
30 (B) CLONE: KLR179

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

35 GCGCAAGCTT CTGCTCGGAC ACCAGAAATG CCTGTT

36

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:  
40 (A) LENGTH: 30 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

45 (vii) IMMEDIATE SOURCE:  
(B) CLONE: KLR180

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

GGCCAAGCTT GCCATTAAGT CTGGTTGCTA

30

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 20 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vii) IMMEDIATE SOURCE:  
    (B) CLONE: MB32

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

AATTCGAGCT CGCCCAAATC

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 40 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vii) IMMEDIATE SOURCE:  
    (B) CLONE: MB37

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

TGAGTAATTT TCGGTGCAGC ACCTCCTACG ACTTGTTCA

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 23 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vii) IMMEDIATE SOURCE:  
    (B) CLONE: RW58

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

TACGCGCAAG AACAGACAAA ATC

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 40 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:  
(B) CLONE: MB38

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

TGAGTAATTT TCGGTGCAGC TCCTCCGTTA GCTTCTGAAA

40

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:  
(B) CLONE: MB39

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

TACGAATTCG AGCTCGCCC

19

(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 76 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:  
(B) CLONE: MB42

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:



ATTTTCGGTG CAGCACCTCC AGAAACAGAA TCTAATTCAT TTAGAGTCAG AGTTCTCATA 60  
ATAACTTTCC TCTTTT 76

5 (2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 40 base pairs  
    (B) TYPE: nucleic acid  
10      (C) STRANDEDNESS: single  
        (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- 15 (vii) IMMEDIATE SOURCE:  
    (B) CLONE: MB41

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

TGAGTAATTT TCGGTGCAGC CATAATAACT TTCCTCTTTT 40

25 (2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 37 base pairs  
    (B) TYPE: nucleic acid  
30      (C) STRANDEDNESS: single  
        (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- 35 (vii) IMMEDIATE SOURCE:  
    (B) CLONE: MB43

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

ATATCACGCC CTGAAGCACC TCCTACGACT TGTTCTGA 37

(2) INFORMATION FOR SEQ ID NO:51:

- 45 (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 36 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
50      (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vii) IMMEDIATE SOURCE:

(B) CLONE: MB44

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

5 AATTAAGCTT GGATCCTTCT GTGTGGATTG TCCAAT 36

(2) INFORMATION FOR SEQ ID NO:52:

10 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: cDNA

20 (vii) IMMEDIATE SOURCE:  
(B) CLONE: APO-1

(ix) FEATURE:  
(A) NAME/KEY: misc\_difference  
(B) LOCATION: replace(11..12, "")  
25 (D) OTHER INFORMATION: /standard\_name= "(any base)"

(ix) FEATURE:  
(A) NAME/KEY: misc\_difference  
(B) LOCATION: replace(16..17, "")  
30 (D) OTHER INFORMATION: /standard\_name= "(any base)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

35 AAAGATATTG GAAAGGATTG G 21